WE CLAIM:

1. A process for identifying a compound which inhibits viral replication that includes contacting nucleic acids from a virus infected host with an amplification reaction mixture that contains at least two primers and/or probes that provide detectable signals during a polymerase chain reaction, wherein

the first primer and/or probe provides a detectable signal on the occurrence of the transcription of viral nucleic acids; and

the second primer and/or probe provides a second detectable signal on the occurrence of the transcription of host nucleic acids.

2. The process of claim 1, wherein the host nucleic acid is nuclear nucleic acid.

3. The process of claim 1, wherein the host nucleic acid is mitochondrial nucleic acid.

4. The process of claim 3, wherein the mitochondrial nucleic acid is mitochondrial DNA.

5. The process of claim 3, wherein the mitochondrial nucleic acid is mitochondrial RNA.

6. The process of claim 1, wherein the viral nucleic acid is a non-coding sequence.

7. The process of claim 6, wherein the non-coding sequence is a 5'-non-coding sequence.

8. The process of claim 6, wherein the non-coding sequence is a 3'-non-coding sequence.

9. The process of claim 6, wherein the non-coding sequence is an intron.

10. The process of claim 6, wherein the non-coding sequence is from β-actin.

11. The process of claim 6, wherein the non-coding sequence is from GAPDH.

12. The process of claim 1, wherein the viral nucleic acid is a coding sequence.

13. The process of claim 12, wherein the coding sequence is from HIV.

14. The process of claim 12, wherein the coding sequence is from HBV.

15. The process of claim 12, wherein the coding sequence is from HCV.

16. The process of claim 12, wherein the coding sequence is from BVDV.

17. The process of claim 12, wherein the coding sequence is from West Nile Virus.

18. The process of claim 12, wherein the coding sequence is from herpes.

19. The process of claim 12, wherein the coding sequence is from influenza.

20. The process of claim 12, wherein the coding sequence is from RSV.

21. The process of claim 12, wherein the coding sequence is from EBV.

22. The process of claim 12, wherein the coding sequence is from CMV.

23. A process for assessing the toxicity of a compound that includes contacting nucleic acids from a host with an amplification reaction mixture that contains at least two primers and/or probes that provide detectable signals during a polymerase chain reaction, wherein

the first primer and/or probe provides a detectable signal on the occurrence on the transcription of host mitochondrial nucleic acids; and

the second primer and/or probe provides a second detectable signal on the occurrence on the transcription of host nuclear nucleic acid.

24. The process of claim 23, wherein the host mitochondrial nucleic acid is mitochondrial DNA.

25. The process of claim 23, wherein the host mitochondrial nucleic acid is mitochondrial RNA.

26. The process of claim 23, wherein the host mitochondrial nucleic acid is a non-coding sequence.

27. The process of claim 26, wherein the non-coding sequence is a 5'-non-coding sequence.

28. The process of claim 26, wherein the non-coding sequence is a 3'-non-coding sequence.

29. The process of claim 26, wherein the non-coding sequence is an intron.

30. The process of claim 26, wherein the non-coding sequence is from β-actin.

31. The process of claim 26, wherein the non-coding sequence is from GAPDH.

32. The process of claim 23, wherein the host mitochondrial nucleic acid is a coding sequence.